

Search #3

seq1.rag

No help, too open world w/ X option page 1

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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 67 Seconds  
(without alignments)  
42.833 Million cell updates/sec

Title: SBO1  
Perfect score: 51  
Sequence: 1 xcycwkvt 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872999 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq23SeqP04; \*  
1: geneseqp1980s; \*\*  
2: geneseqp1990s; \*\*  
3: geneseqp200s; \*\*  
4: geneseqp2001s; \*\*  
5: geneseqp2002s; \*\*  
6: geneseqp2003as; \*\*  
7: geneseqp2004s; \*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	51	100.0	8 1	AAP61464
2	51	100.0	8 1	AAP71379
3	51	100.0	8 1	AAP71378
4	51	100.0	8 1	AAP71378
5	51	100.0	8 2	AAPR07024
6	51	100.0	8 2	AAPR07021
7	51	100.0	8 2	AAPR07022
8	51	100.0	8 2	AAPR05192
9	51	100.0	8 2	AAPR14234
10	51	100.0	8 2	AAPR14226
11	51	100.0	8 2	AAPR10504
12	51	100.0	8 2	AAPR26371
13	51	100.0	8 2	AAPR26370
14	51	100.0	8 2	AAPR27177
15	51	100.0	8 2	AAPR27178
16	51	100.0	8 2	AAPR27190
17	51	100.0	8 2	AAPR23951
18	51	100.0	8 2	AAPR40816
19	51	100.0	8 2	AAPR41505
20	51	100.0	8 2	AAPR41501
21	51	100.0	8 2	AAPR31510
22	51	100.0	8 2	AAPR42656
23	51	100.0	8 2	AAPR56780
24	51	100.0	8 2	AAPR56709
25	51	100.0	8 2	AAPR56778

RESULT 1			
ID	AAP61464	standard; protein;	8 AA.
XX			
AC	AAP61464;		
XX			
DT	25-MAR-2003	(revised)	
DT	27-OCT-1991	(First entry)	
XX			
DE	Cyclic octapeptide somatostatin analogue.		
XX			
KW	Growth hormone; prolactin; insulin; glucagon; gastrin; secretin; Cholecystokinin.		
XX			
OS	Synthetic.		
XX			
FT	Key	Location/Qualifiers	
FT	Modified-site	1 /label= D-Phe	
FT	Disulfide-bond	2 .7	
FT	Modified-site	4 .7	
FT	/label= D-Trp		
XX			
PN	EP203031-A.		
XX			
PD	26-NOV-1986.		
XX			
PP	15-APR-1986;	86RP-00810174..	
XX			
PR	25-APR-1985;	85TS-00727105..	
PR	28-MAR-1986;	860S-00843539..	
PR			
PA	(TULSA ) TULANE EDUCATIONAL FUND.		
XX			
PI	Schally AV, Cai RZ;		
XX			
DR	WPI: 1986-313466/48.		
XX			
PT	New cyclic octa-peptide somatostatin analogues - and reduced linear intermediates.		
XX			
PS	Claim 8; Page 31; 33pp; English.		
XX			

Somatostatin analogues inhibit the release of growth hormone, prolactin, insulin, gastrin, secretin and cholecystokinin. They also, may be used in treatment of diabetic retinopathy, diabetes, ulcers, acute pancreatitis and agromegaly. The analogues may also be used in treating prostatic

CC adeno-carcinomas, mammary carcinomas, insulinomas, gastrinomas and growth  
 CC hormone and insulin dependent tumours. (Updated on 25-MAR-2003 to correct  
 PA field.)  
 XX SQ Sequence 8 AA;

Query Match	100.0%	Score	51	DB	1	Length	8
Best Local Similarity	87.5%	Pred. No.	1.7e+06				
Matches	7	Conservative	1	Mismatches	0	Indels	0
Gaps	0						

OY 1 XCYWKVCT 8  
 DB 1 FCYWKVCT 8

**RESULT 2**

AAP71379	100.0%	Score	51	DB	1	Length	8
ID	AAP71379	standard; peptide; 8 AA.					
XX							
AC	AAP71379;						
XX							
DT	09-SEP-2004 (revised) 25-MAR-2003 (revised)						
DT	03-OCT-2002 (first entry)						
XX							
DE	Sequence of somatostatin analogue.						
XX							
KW	Growth hormone secretion inhibitor; cancer therapy; Alzheimer's disease; KW diabetes.						
XX							
OS	Synthetic.						
XX							
FH	Key Location/Qualifiers						
FT	Misc-difference 1 /label= pentafluoro-D-Phe						
FT	Misc-difference 4 /label= D-TIP						
FT	Misc-difference 8 /label= Thr-NH2						
XX							
PN	EP14872-A.						
XX							
PD	18-MAR-1987.						
XX							
PF	12-SEP-1986; 86EP-00307044.						
XX							
PR	12-SEP-1985; 86US-00775488.						
PR	17-JUN-1986; 86US-00875266.						
PR	22-JUN-1988; 88US-0020983.						
PA	(TULANE ) TULANE EDUCATIONAL FUND FUND.						
XX							
PI	Coy DH, Murphy WA, Heman ML;						
XX							
DR	WPI; 1987-074173/11.						
XX							
PT	Somatostatin analogue octa-peptide(s) with enhanced activity - are useful in the rxn. of growth hormone, insulin glucagon, or pancreatic exocrine secretion, and have anticancer activity.						
PT	disclosure; Page; 10pp; English.						
PS	They are administered in somatostatin dosages or because of their greater potency, in smaller dosages. Dosage is 0.01-1000 mcg./kg./day pref. 0.1- 100 mcg./kg./day to mammal eg human. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)						
CC	Revised record issued on 09-SEP-2004 : Correction to sequence location						
CC	Sequence 8 AA;						

CC Query Match 100.0%; Score 51; DB 1; Length 8;  
 CC Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
 CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC SQ Sequence 8 AA;

Query Match	100.0%	Score	51	DB	1	Length	8
Best Local Similarity	87.5%	Pred. No.	1.7e+06				
Matches	7	Conservative	1	Mismatches	0	Indels	0
Gaps	0						

OY 1 XCYWKVCT 8  
 DB 1 FCYWKVCT 8

**RESULT 3**

AAP71378	100.0%	Score	51	DB	1	Length	8
ID	AAP71378	standard; peptide; 8 AA.					
XX							
AC	AAP71378;						
XX							
DT	09-SEP-2004 (revised) 25-MAR-2003 (revised)						
DT	03-OCT-2002 (revised)						
DT	03-MAY-1991 (first entry)						
DE	Sequence of somatostatin analogue.						
XX							
KW	Growth hormone secretion inhibitor; cancer therapy; Alzheimer's disease; KW diabetes.						
XX							
OS	Synthetic.						
XX							
FH	Key Location/Qualifiers						
FT	Misc-difference 1 /label= D-beta-Nal						
FT	Misc-difference 4 /label= D-TIP						
FT	Misc-difference 8 /label= Thr-NH2						
XX							
PN	BP214872-A.						
XX							
PD	18-MAR-1987.						
XX							
PP	12-SEP-1986; 86EP-00307044.						
XX							
PR	12-SEP-1985; 86US-00775488.						
PR	17-JUN-1986; 86US-00875266.						
PR	22-JUN-1988; 88US-0020983.						
PA	(TULANE ) TULANE EDUCATIONAL FUND FUND.						
XX							
PI	Coy DH, Murphy WA, Heman ML;						
XX							
DR	WPI; 1987-074173/11.						
XX							
PT	Somatostatin analogue octa-peptide(s) with enhanced activity - are useful in the rxn. of growth hormone, insulin glucagon, or pancreatic exocrine secretion, and have anticancer activity.						
PT	disclosure; Page; 10pp; English.						
PS	They are administered in somatostatin dosages or because of their greater potency, in smaller dosages. Dosage is 0.01-1000 mcg./kg./day pref. 0.1- 100 mcg./kg./day to mammal eg human. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)						
CC	Revised record issued on 09-SEP-2004 : Correction to sequence location						
CC	Sequence 8 AA;						

QY 1 XCYWKVCT 8  
DB 1 XCYWKVCT 8

**RESULT 4**

ID AAR07024 standard; protein; 8 AA.  
XX  
AC AAR07024;  
XX DT 21-JAN-1991 (first entry)  
XX DE Octapeptide somatostatin analogue.  
XX KW Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;  
XX hepatitis; insulin; glucagon.  
XX OS Synthetic.

Key Location/Qualifiers  
FT Modified-site /label= OTHER, Dextrorotatory  
FT /notes= "D-beta-Nal"  
FT Modified-site 3 /label= Iodinated phenyl ring  
FT Modified-site 4 /label= Dextrorotatory  
FT EP389180-A.  
PN XX  
PD XX 26-SEP-1990.  
FT XX 15-MAR-1990; 90EP-00302760.  
PR XX 15-MAR-1989; 89US-00323777.  
PA XX (BIOM-) BIOMEASURE INC.  
PT XX Beck CR, Moreau S;  
DR XX WPI; 1990-292105/39.  
PT XX New octa:peptide somatostatin analogues - useful for treating diabetes,  
XX liver disease, growth hormone dependent cancer, alzheimers disease etc.  
PS XX Claim 5; Page 5; 8pp; English.  
CC XX Analogues to somatostatin, useful for reducing or inhibiting release of  
CC antagonising growth hormone, insulin, glucagon or pancreatic exocrine  
CC solution. The peptides can treat diabetes related retinopathy, cirrhosis,  
CC hepatitis, Alzheimer's disease, cancers etc  
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;  
Best Local Similarity 100.0%; Prod. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
DB 1 XCYWKVCT 8

**RESULT 6**

ID AAR07022  
XX AAR07022 standard; protein; 8 AA.  
XX AC AAR07022;  
XX DT 21-JAN-1991 (first entry)  
XX DE Octapeptide somatostatin analogue.  
XX KW Growth hormone dependent cancer; diabetes; Alzheime's disease; Cirrhosis;  
XX hepatitis; insulin; glucagon.  
XX OS Synthetic.

Key Location/Qualifiers  
FT Modified-site 1 /label= Dextrorotatory  
FT /notes= "Pentafluoro-D-Phe"  
FT Modified-site 3 /label= Iodinated phenyl ring  
FT Modified-site 4 /label= Dextrorotatory

RESULT 5  
AAR07021  
ID AAR07021 standard; protein; 8 AA.  
XX AC AAR07021;  
XX DT 21-JAN-1991 (first entry)  
XX DE Octapeptide somatostatin analogue.

XX  
PN BP389180-A.  
XX  
PD 26-SEP-1990.  
XX  
PF 15-MAR-1990; 90EP-00302760.  
XX  
PR 15-MAR-1989; 89US-00323777.  
XX  
PA (BIOM-) BIOMEASURE INC.  
XX  
PI Eck CR.; Moreau S;  
XX  
DR WPI; 1990-292105/39.  
XX  
PT New octapeptide somatostatin analogues - useful for treating diabetes,  
PT liver disease, growth hormone dependent cancer, alzheimers disease etc.  
XX  
PS Claim 5; 8pp; English.  
XX  
CC Analogues to somatostatin, useful for reducing or inhibiting release of  
CC taotaonising growth hormone, insulin, glucagon or pancreatic exocrine  
CC solution. The Peptides can treat diabetes related retinopathy, cirrhosis,  
CC hepatitis, Alzheimer's disease, cancers etc  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;  
Best local Similarity 87.5%; Pred. No. 1.7e-06; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 0;

QY 1 XCYWKVCT B  
Db 1 FCYWVKCT B

RESULT 7  
AAR05192  
ID AAR05192 standard; protein; 8 AA.  
XX  
AC AAR05192;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAR-2003 (revised)  
DT 11-OCT-1990 (first entry)  
XX  
DE Somatostatin analogue or deriv. used as lung damage protectant.  
XX  
KW Somatostatin analog; lung damage protection; respiratory distress syndrome;  
XX  
OS Homo sapiens.

XX  
PH Key  
PT Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "D-Phe which carries 2,3-diaminopropionic acid(4-  
FT Disulfide-bond 2. .7  
[bis(2-chlorethyl)amino]Phe)2 cytotoxic moiety"  
XX  
PN BP450480-A.  
XX  
PD 09-OCT-1991.  
XX  
PP 27-MAR-1991; 91EP-00104845.  
XX  
PR 06-APR-1990; 90US-00505501.  
XX  
PA (TULANE EDUCATIONAL FUND.  
PA (SCHA/) SCHALLY A V.  
XX  
PI Schally AV, Janaky T, Cai RZ;  
XX  
WPI; 1991-297292/41.  
XX  
DR  
XX  
PT New cyclic somatostatin peptide derivatives - have cytotoxic activity,  
PT used for treating certain cancers e.g. adeno and mammary carcinoma(s),  
PT gastric cancers, brain tumours, etc.  
XX  
Claim 9; Page 9 and Page 27; 28pp; English.  
XX  
CC The C-terminus is amidated and Phe(1) and Trp(4) are in the D-  
CC configuration. This peptide is a specific example of a generic formula.  
CC It inhibits secretion of pituitary GH and has neoplastic effect. It is  
CC useful for treatment of hormone-sensitive tumours. See AAR14225-R14238.

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XX  
PS Disclosure; Page ?; -pp; German.  
XX  
CC Residues A at positions 1 is beta-Naphthyl-(D)-Alanine and residue Trp at  
position 4 is D-Trp. Derivs of this sequence subsed. on the N-terminal  
CC amino GP. by N alpha-(alpha-glucosyl-(1-4)deoxyfructosyl) or N alpha-(beta-  
CC -deoxyfructosyl) are pref for oral administration. The cpds. are esp.  
CC used to prevent, inhibit or treat respiratory distress syndrome in  
CC children and adults, and to inhibit or treat lung damage caused by oxygen  
CC therapy. Opt. they are formulated with a glucocorticoid steroid. They  
CC are also known to inhibit release of growth hormone, insulin, and  
CC glucagon, and to reduce gastric secretions. See also AAR0577-80,  
CC AAR05182-88, AAR05191-95, AAR0530 and AAR0197. (Updated on 10-MAR-2003  
CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;  
Best local Similarity 87.5%; Pred. No. 1.7e-06; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 0;

QY 1 XCYWKVCT B  
Db 1 ACYWVKCT B

RESULT 8  
AAR14234  
ID AAR14234 standard; protein; 8 AA.  
XX  
AC AAR14234;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-DEC-1991 (first entry)  
XX  
DE Somatostatin deriv. #9 contg. cytotoxic moiety.  
XX  
KW pituitary growth hormone; GH; antineoplastic.  
XX  
OS Synthetic.

XX  
PH Key  
PT Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "D-Phe which carries 2,3-diaminopropionic acid(4-  
FT Disulfide-bond 2. .7  
[bis(2-chlorethyl)amino]Phe)2 cytotoxic moiety"  
XX  
PN BP450480-A.  
XX  
PD 09-OCT-1991.  
XX  
PP 27-MAR-1991; 91EP-00104845.  
XX  
PR 06-APR-1990; 90US-00505501.  
XX  
PA (TULANE EDUCATIONAL FUND.  
PA (SCHA/) SCHALLY A V.  
XX  
PI Schally AV, Janaky T, Cai RZ;  
XX  
WPI; 1991-297292/41.  
XX  
DR  
XX  
PT New cyclic somatostatin peptide derivatives - have cytotoxic activity,  
PT used for treating certain cancers e.g. adeno and mammary carcinoma(s),  
PT gastric cancers, brain tumours, etc.  
XX  
Claim 9; Page 9 and Page 27; 28pp; English.  
XX  
CC The C-terminus is amidated and Phe(1) and Trp(4) are in the D-  
CC configuration. This peptide is a specific example of a generic formula.  
CC It inhibits secretion of pituitary GH and has neoplastic effect. It is  
CC useful for treatment of hormone-sensitive tumours. See AAR14225-R14238.

(Updated on 25-MAR-2003 to correct PA field.)

CC ID AAR10504 standard; protein; 8 AA.  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+06; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCWVKVCT 8  
 :|||||||  
 Db 1 FCWVKVCT 8

RESULT 9

ARR14226 ID AAR14226 standard; protein; 8 AA.  
 XX  
 AC AAR14226;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-MAR-2003 (revised)  
 DT 09-APR-1991 (first entry)

DE Pamamate of somatostatin octapeptide.

XX Sustained release peptide compn; lactic acid; glycolic acid;  
 KW somatostatin; luteinising hormone releasing hormone.

XX Unidentified.

OS

XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1;.1  
 FT /label= Phe= D-Phe  
 FT Disulfide-bond 2;.7  
 FT Modifiedsite 4;.4  
 FT /label= Trp= D-Trp

FT  
 XX  
 PN GB2234169-A.  
 XX  
 PD 30-JAN-1991.  
 XX  
 PP 17-JUL-1990; 90GB-0001572.  
 XX  
 PR 28-JUL-1989; 89CH-00002829.  
 XX  
 PA (DEBI-) DEBIOPHARM SA.  
 XX  
 PX Orsolini P,  
 XX  
 DR WPI; 1991-031530/05.

XX  
 PR Sustained release pharmaceutical peptide compn. prepn. - involves  
 PT preheating and compressing mixt. of lactic and glycolic acid copolymers  
 PT with active substance pamamate, etc.

XX  
 PS Claim 9; Page 12; 14pp; English.

XX  
 CC This peptide is used as the active substance in a pharmaceutical compn.  
 CC for sustained release of somatostatin. It is mixed with a lactic  
 CC acid/glycolic acid co-polymer. All components are in the form of  
 CC microparticles and an injectable soln. is obt. See also AAR10501-03 and  
 CC AAR10505-09. (Updated on 10-MAR-2003 to add missing OS field.) (Updated  
 CC on 25-MAR-2003 to correct PA field.)

XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+06; 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCWVKVCT 8  
 :|||||||  
 Db 1 FCWVKVCT 8

RESULT 11

ARR26371 ID ARR26371 standard; peptide; 8 AA.  
 XX  
 AC AAR26371;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-FEB-1993 (first entry)

XX  
 DE Somatostatin analogue.

XX  
 KW Skin disease; melanoma; keratosis; basal cell epithelial pagetoid;  
 KW basal cell carcinoma; non toxic.

RESULT 10

ARR10504

XX OS Synthetic.

XX OS Synthetic.

FT Location/Qualifiers

Key Misc-difference 1 /note= "D-beta-naphthylalanine"

FT Disulfide-bond 2 . 7

FT Misc-difference 4 /note= "D-Trp"

FT Modified-site 8 /note= "amidated"

XX PN WO9213554-A1.

XX PD 20-AUG-1992.

XX PR 07-FEB-1992; 92WO-US001027.

XX PR 08-FEB-1991; 91US-00652863.

PA (BIOM-) BIOMEASURE INC.

XX PA Bogden AE, Moreau J;

PI DR WPI; 1992-299754/36.

XX PT Anti-proliferative compsn. comprising somatostatin analogue - used to treat benign and malignant proliferative skin diseases e.g. melanomas.

XX CC The peptide is an example of a somatostatin analogue used to treat melanoma and their malignant skin metastases (these express somatostatin receptors), recurring keratosis, non-invasive basal cell epithelial pagetoid and basal cell carcinoma. Peptides have 4 (pref. 6 or 7) amino acids with at least 20 (pref. 50) percent homology with the core region of somatostatin and has a D-Trp at position 4. See also AAR26367-74. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

PS Claim 10; Page 16; 25pp; English.

XX CC The Peptide is an example of a somatostatin analogue used to treat melanomas and their malignant skin metastases (these express somatostatin receptors), recurring keratosis, non-invasive basal cell epithelial pagetoid and basal cell carcinoma. Peptides have 4 (pref. 6 or 7) amino acids with at least 20 (pref. 50) percent homology with the core region of somatostatin and has a D-Trp at position 4. See also AAR26367-74. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

CC Query Match Score 51; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8

Db 1 XCYWKVCT 8

RESULT 12

ID AAR26370 standard; peptide; 8 AA.

XX AC AAR27177; ID AAR27177 standard; peptide; 8 AA.

XX AC AAR27177; DT 09-SEP-2004 (revised)

XX DT 25-MAR-2003 (revised)

DT 21-MAY-1998 (first entry)

DE Somatostatin analogue tyrosine kinase inhibitor #1.

XX KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of; KW release of; growth hormone; insulin; glucagon; prolactin; KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "beta-aspartyl", where alpha-carboxy group forms amide with indoline"

FT Disulfide-bond 2 . 7

FT Misc-difference 4 /note= "D-form"

FT Modified-site 8 /note= "amidated"

XX FN EP505680-A1.

XX PD 30-SEP-1992.

XX PR 27-JAN-1992; 92EP-00101196.

XX XX XX PR XX PA XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.  
 XX PA XX PI Keri G, Mezoe I, Horvath A, Vadasz Z, Tepian I, Balogh A;  
 PA CSuka O, Boekoenyi G, Szoeke B, Horvath J, Idei M, Seprodi J;  
 PI DR XX WPI; 1992-325051/40.  
 PT XX PT New octa:peptide or hepta:peptide somastatin analogues - as tyrosine  
 PT kinase inhibitors for treating tumours and psoriasis, and for regulating  
 PT hormone release.  
 XX PS XX Claim 5; Page 30; 36pp; English.  
 CC This peptide is a somatostatin analogue showing more advantageous and  
 selective pharmacological action than somatostatin. It has a structure  
 inhibiting the activity of exopeptidases. It can be used in medicaments  
 to inhibit tumour growth or the activity of tyrosine kinase enzymes  
 involved in tumour transformation. It is also useful for regulating the  
 release of growth hormone, insulin, glucagon and prolactin. It may also  
 be used to inhibit pathological processes such as psoriasis, elicited by  
 the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to  
 correct PN field.)  
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key  
 CC SQ Sequence 8 AA:  
 Query Match 100.0%; Score 51; DB 2; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XCYWKVCT 8  
 DB 1 DCYWKVCT 8  
 RESULT 14  
 AAR27178 ID AAR27178 standard; peptide; 8 AA.  
 XX AC AAR27178;  
 XX DT 09-SEP-2004 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 21-MAY-1998 (first entry)  
 XX DE Somatostatin analogue tyrosine kinase inhibitor #2.  
 XX DE tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;  
 KW release of; growth hormone; insulin; glucagon; prolactin;  
 KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.  
 XX OS Synthetic.  
 XX  
 PH Key  
 FT Misc-difference 1 /note= "D-form"  
 FT Disulfide-bond 2 .7  
 FT Misc-difference 4 /note= "D-form"  
 FT Modified-site 8 /note= "amidated"  
 FT Modified-site 1 /label= OTHER  
 FT Disulfide-bond /note= "D-tetrahydroisoquinoline carboxylic acid (D-TIC)"  
 FT Misc-difference 4 /note= "D-form"  
 FT Modified-site 8 /note= "amidated"  
 XX PN EP505680-A1.  
 XX PD 30-SEP-1992.  
 XX PF 27-JAN-1992; 92EP-00101196.  
 XX PR 25-JAN-1991; 91HU-00000272.  
 XX  
 XX XX XX PR XX PA XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.  
 XX PA XX PI Keri G, Mezoe I, Horvath A, Vadasz Z, Tepian I, Balogh A;  
 PA CSuka O, Boekoenyi G, Szoeke B, Horvath J, Idei M, Seprodi J;  
 PI DR XX WPI; 1992-325051/40.  
 PT XX PT New Octa:peptide or hepta:peptide somastatin analogues - as tyrosine  
 PT kinase inhibitors for treating tumours and psoriasis, and for regulating  
 PT hormone release.  
 XX PS XX Claim 5; Page 30; 36pp; English.  
 CC This peptide is a somatostatin analogue showing more advantageous and  
 selective pharmacological action than somatostatin. It has a structure  
 inhibiting the activity of exopeptidases. It can be used in medicaments  
 to inhibit tumour growth or the activity of tyrosine kinase enzymes  
 involved in tumour transformation. It is also useful for regulating the  
 release of growth hormone, insulin, glucagon and prolactin. It may also  
 be used to inhibit pathological processes such as psoriasis, elicited by  
 the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to  
 correct PN field.)  
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key  
 CC SQ Sequence 8 AA:  
 Query Match 100.0%; Score 51; DB 2; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XCYWKVCT 8  
 DB 1 FCYWKVCT 8  
 RESULT 15  
 AAR27188 ID AAR27188 standard; peptide; 8 AA.  
 XX AC AAR27188;  
 XX DT 09-SEP-2004 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 21-MAY-1998 (first entry)  
 XX DE Somatostatin analogue tyrosine kinase inhibitor #12.  
 XX DE tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;  
 KW release of; growth hormone; insulin; glucagon; prolactin;  
 KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.  
 XX OS Synthetic.  
 XX  
 PH Key  
 FT Modified-site 1 /label= OTHER  
 FT Disulfide-bond /note= "D-tetrahydroisoquinoline carboxylic acid (D-TIC)"  
 FT Misc-difference 4 /note= "D-form"  
 FT Modified-site 8 /note= "amidated"  
 XX PN EP505680-A1.  
 XX PD 30-SEP-1992.  
 XX PF 27-JAN-1992; 92EP-00101196.  
 XX PR 25-JAN-1991; 91HU-00000272.

PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.  
 XX  
 PI Keri G, Mazoe I, Horvath A, Vadász Z, Tepán I, Baloch A;  
 PI Csuka O, Boekonyi G, Szőke B, Horváth J, Idei M, Seprodi J;  
 XX DR WPI; 1992-325051/40.  
 XX PT New octapeptide or hepta-peptide somatostatin analogues - as tyrosine  
 PT kinase inhibitors for treating tumours and psoriasis, and for regulating  
 PT hormone release.  
 XX  
 PS Example 11; Page 23; 36PP; English.  
 XX  
 CC This peptide is a somatostatin analogue showing more advantageous and  
 CC selective pharmacological action than somatostatin. It has a structure  
 CC inhibiting the activity of exopeptidases. It can be used in medicaments  
 CC to inhibit tumour growth or the activity of tyrosine kinase enzymes  
 CC involved in tumour transformation. It is also useful for regulating the  
 CC release of growth hormone, insulin, glucagon and prolactin. It may also  
 CC be used to inhibit pathological processes such as psoriasis, elicited by  
 CC the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key  
 XX SQ Sequence 8 AA;  
 Query Match 100.0%; Score 51; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XCYWKVCT 8  
 Db 1 XCYWKVCT 8

Search completed: November 18, 2004, 16:22:33  
 Job time : 69 secs

Copyright GenCore version 5.1.6  
 (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:39 ; Search time 21 Seconds  
 (without alignments)

Title: SEQ1  
 Perfect score: 51  
 Sequence: 1 xcxywkvt 8

Scoring table: BLOSUM62DX  
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB\_pep: \*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB\_pep: \*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB\_pep: \*  
 5: /cgn2\_6/ptodata/1/iaa/PCTMUS\_COMB\_pep: \*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
1	51	100.0	8	1 US-08-286-748B-7	Sequence 7, Appli
2	51	100.0	8	3 US-08-586-670A-13	Sequence 13, Appli
3	51	100.0	8	14 US-08-586-14	Sequence 14, Appli
4	51	100.0	8	4 US-08-528-200-157	Sequence 157, Appli
5	51	100.0	9	3 US-08-586-670A-11	Sequence 11, Appli
6	51	100.0	9	3 US-08-586-670A-15	Sequence 15, Appli
7	47	92.2	8	3 US-09-484-318-1	Sequence 1, Appli
8	47	92.2	8	3 US-09-484-318-8	Sequence 8, Appli
9	47	92.2	8	3 US-09-484-319-1	Sequence 1, Appli
10	47	92.2	8	3 US-09-484-319-8	Sequence 8, Appli
11	47	92.2	8	3 US-09-484-320-1	Sequence 1, Appli
12	47	92.2	8	3 US-09-484-320-8	Sequence 8, Appli
13	47	92.2	8	3 US-09-484-321-1	Sequence 1, Appli
14	47	92.2	8	3 US-09-484-323-1	Sequence 1, Appli
15	47	92.2	8	3 US-09-484-323-8	Sequence 8, Appli
16	47	92.2	8	3 US-09-484-329-1	Sequence 1, Appli
17	47	92.2	8	3 US-09-528-200-156	Sequence 159, Appli
18	47	92.2	8	3 US-09-528-200-159	Sequence 13, Appli
19	47	92.2	8	3 US-09-636-170-8	Sequence 3, Appli
20	47	92.2	8	3 US-09-636-170-8	Sequence 1, Appli
21	47	92.2	8	3 US-09-637-518-1	Sequence 8, Appli
22	47	92.2	8	4 US-09-637-518-8	Sequence 156, Appli
23	47	92.2	8	4 US-09-528-200-156	Sequence 159, Appli
24	46	90.2	9	3 US-08-985-526-13	Sequence 13, Appli
25	46	90.2	9	3 US-08-985-526-13	Sequence 3, Appli
26	46	90.2	3	3 US-08-985-526-13	Sequence 3, Appli
27	46	90.2	3	3 US-09-194-296-3	Sequence 3, Appli

RESULT 1  
 US-08-286-748B-7  
 Sequence 7, Application US/08286748B  
 Patent No. 5759542

GENERAL INFORMATION:

APPLICANT: Victor Gurevich

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY OF DRUGS BY PLATELETS FOR THE TREATMENT OF CARDIOVASCULAR AND OTHER DISEASES

TITLE OF INVENTION: NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM PS/2 Model 50Z or 55SX  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: Wordperfect (version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286-748B  
 FILING DATE: August 5, 1994  
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: J. Peter Fasse  
 REGISTRATION NUMBER: 32,983  
 REFERENCE DOCKET NUMBER: 04547/013001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-0700  
 TELEFAX: (617) 542-8906  
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 8

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE: OTHER INFORMATION: Xaa is D- Naphthylalanine

Query Match 100.0%; Score 51; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
Db 1 XCYWKVCT 8

RESULT 2  
US-08-586-670A-13  
Sequence 13, Application US/08586670A  
Patent No. 6241965  
GENERAL INFORMATION:  
APPLICANT: McBride, William  
APPLICANT: Dean, Richard T.  
TITLE OF INVENTION: Somatostatin Derivatives  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSE: Banner & Witcoff, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,670A  
FILING DATE: 22-APR-1996  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: No. 6241965ian, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,385-DD

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids

REFERENCE/DOCKET NUMBER: 92,385-DD

TELEPHONE: 312-715-1000  
TELEFAX: 910-221-5317

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..4  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked  
to DTPA; Trp is in the D conformation;"  
US-08-586-670A-13

Query Match 100.0%; Score 51; DB 3; Length 8;  
Best Local Similarity 100.0%; Score 51; DB 3; Length 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8  
Db 1 XCYWKVCT 8

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RESULT 3  
US-08-586-670A-14  
Sequence 14, Application US/08586670A  
Patent No. 6241965  
GENERAL INFORMATION:  
APPLICANT: McBride, William  
APPLICANT: Dean, Richard T.  
TITLE OF INVENTION: Somatostatin Derivatives  
TITLE OF INVENTION: And their Radiolabeled Products  
NUMBER OF SEQUENCES: 23

QY 1 XCYWKVCT 8  
Db 1 XCYWKVCT 8

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RESULT 4  
US-09-528-200-157  
Sequence 157, Application US/09528200  
Patent No. 6330570  
GENERAL INFORMATION:  
APPLICANT: LICHA, KAI  
APPLICANT: BECKER, ANDREAS  
APPLICANT: SEMMLER, WOLFGARD  
APPLICANT: WEIDENMANN, BERTRAM  
APPLICANT: HESSENJUS, CARSTEN  
APPLICANT: VOLMER-ENGERT, RUDOLF  
APPLICANT: SCHNEIDER-MERGNER, JENS  
APPLICANT: BHARGAVA, SARAH  
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA  
FILE REFERENCE: SCH-1731  
CURRENT APPLICATION NUMBER: US/09/528,200  
CURRENT FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: DE 199 17 713-9  
PRIOR FILING DATE: 1999-09-04  
NUMBER OF SEQ ID NOS: 196  
SOFTWARE: Patentin Ver. 2.1  
SBO ID NO: 157  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-09-528-200-157  
 ;  
 ; OTHER INFORMATION: peptide

RESULT 5  
 Query Match 100.0%; Score 51; DB 4; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 3. 8e+05; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0;  
 QY 1 XCYWKVCT 8  
 Db :||||||| 1 FCYWKVCT 8

RESULT 6  
 US-08-586-670A-15  
 Sequence 15 Application US/08586670A  
 Patent No. 6241965  
 GENERAL INFORMATION:  
 APPLICANT: McBride, William T.  
 APPLICANT: Dean, Richard T.  
 TITLE OF INVENTION: Somatostatin Derivatives  
 TITLE OF INVENTION: And their Radiolabeled Products  
 NUMBER OF SEQUENCES: 23  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Banner & Witcoff, Ltd.  
 STREET: 10 South Wacker Drive, Suite 3000  
 CITY: Chicago  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/586,670A  
 FILING DATE: 22-APR-1996  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 6241965n, Kevin E  
 REGISTRATION NUMBER: 35,303  
 REFERENCE/DOCKET NUMBER: 92,385-DD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-715-1000  
 TELEX: 312-715-1234  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1..3  
 OTHER INFORMATION: /label= Variant residues  
 OTHER INFORMATION: /note= "The Lys is linked to a BAT chelator  
 OTHER INFORMATION: through the side chain nitrogen; Xaa is D-naphthylalanine;  
 OTHER INFORMATION: at the N-terminus; Xaa is D-naphthylalanine;  
 OTHER INFORMATION: /note= "The Trp residue is in the D conformation;  
 OTHER INFORMATION: each of the Cys side chain sulfur atoms are methylated;

FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 5..8  
 OTHER INFORMATION: /label= Variant residues  
 OTHER INFORMATION: /note= "The Trp residue is in the D conformation;  
 OTHER INFORMATION: the Cys side chain sulfur is methylated;

FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 3..8  
 OTHER INFORMATION: /label= Variant residues  
 OTHER INFORMATION: /note= "The Trp residue is in the D conformation;  
 OTHER INFORMATION: each of the Cys side chain sulfur atoms are methylated;

Query Match 100.0%; Score 51; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 3. 8e+05; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0;  
 QY 1 XCYWKVCT 8  
 Db 2 XCYWKVCT 9

```

; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL DYES
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFD
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-484-318-1

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8
Db 1 FCYWKVCT 8

RESULT 8
US-09-484-318-8
; Sequence 8, Application US/09484318
; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL DYES
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFD
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
; US-09-484-319-1

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8
Db 1 FCYWKVCT 8

RESULT 10
US-09-484-319-8
; Sequence 8, Application US/09484319
; Patent No. 6180086
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,319
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFD
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This is D-tryptophan
; US-09-484-318-8

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;

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```

; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
US-09-484-319-8

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 XCYWKVCT 8
Db 1 FCYWKVCT 8

RESULT 11
US-09-484-320-1
; Sequence 1, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; FILE REFERENCE: dinstrg
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-320-1

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 XCYWKVCT 8
Db 1 FCYWKVCT 8

RESULT 12
US-09-484-320-8
; Sequence 8, Application US/09484320
; Patent No. 6180087
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Bujaj, Joseph E
; TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
; CURRENT APPLICATION NUMBER: US/09/484,320
; CURRENT FILING DATE: 2000-01-18

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 XCYWKVCT 8
Db 1 FCYWKVCT 8

RESULT 13
US-09-484-321-1
; Sequence 1, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Octreotide
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-phenylalanine
; NAME/KEY: DISULFID
; LOCATION: (2)..(7)
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: This is D-tryptophan
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-321-1

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 XCYWKVCT 8
Db 1 FCYWKVCT 8

RESULT 14
US-09-484-321-8
; Sequence 8, Application US/09484321

```

Patent No. 61983726  
 GENERAL INFORMATION:  
 APPLICANT: Achilefu, Samuel  
 APPLICANT: Rajagopalan, Raghavan  
 APPLICANT: Dorzhow, Richard B.  
 APPLICANT: Bugaj, Joseph E.  
 TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES  
 CURRENT APPLICATION NUMBER: US/09/484,321  
 CURRENT FILING DATE: 2000-01-18  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 8  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Octreotide  
 LOCATION: (1)  
 OTHER INFORMATION: This is D-phenylalanine  
 NAME/KEY: DISULFID :|||  
 LOCATION: (2)..(7)  
 NAME/KEY: SITE  
 LOCATION: (4)  
 OTHER INFORMATION: This is D-tryptophan  
 ;US-09-484-321-8  
 Query Match Similarity 92.2%; Score 47; DB 3; Length 8;  
 Best Local Matches 75.0%; Pred. No. 3.8e+05; 1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Misnmatches 1; Indels 0; Gaps 0;  
 QY 1 XCIWKVCT 8  
 Db 1 FCYWKVCT 8  
 RESULT 15  
 US-09-484-323-1  
 ; Sequence 1, Application US/09484323  
 ; Patent No. 6190641  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Achilefu, Samuel  
 ; APPLICANT: Rajagopalan, Raghavan  
 ; APPLICANT: Dorzhow, Richard B.  
 ; APPLICANT: Bugaj, Joseph E.  
 ; TITLE OF INVENTION: NOVEL INDOCYANINE DYES  
 ; FILE REFERENCE: DNA STRING  
 ; CURRENT APPLICATION NUMBER: US/09/484,323  
 ; CURRENT FILING DATE: 2000-01-18  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 1  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Octreotide  
 NAME/KEY: SITE  
 LOCATION: (1)  
 OTHER INFORMATION: This is D-phenylalanine  
 NAME/KEY: DISULFID :|||  
 LOCATION: (2)..(7)  
 NAME/KEY: SITE  
 LOCATION: (4)  
 OTHER INFORMATION: This is D-tryptophan  
 NAME/KEY: SITE  
 LOCATION: (8)  
 OTHER INFORMATION: This C-terminal residue ends with a hydroxyl  
 ;US-09-484-323-1  
 Query Match 92.2%; Score 47; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 3.8e+05;

	Matches	6;	Conservative	1;	Misnmatches	1;	Indels	0;	Gaps	0;
QY	1	XCIWKVCT	8	:						
Db	1	FCYWKVCT	8							

Search completed: November 18, 2004, 16:21:19  
 Job time : 22 secs

Run on: November 18, 2004, 16:19:39 ; Search time 64 Seconds  
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Om protein - protein search, using sw model

Title: Sequence: Perfect score: Sequence: Scoring table: BLOSUM62DX Gapext 10.0 , Gapext 0.5

Searched: 1 xcywkvt 8

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	44	86.3	468	Q8i619 halocynthia
2	42	82.4	107	Q7PJ80 anophelles g
3	42	82.4	256	Q7R3E2 giardia lam
4	42	82.4	493	P97525 rattus norv
5	42	82.4	498	Q60846 mus musculu
6	42	82.4	826	Q8EIJ1 ocellij shewaneila
7	41	80.4	192	Q99GU2 helicoverpa
8	41	80.4	192	Q9BZ28 helicoverpa
9	41	80.4	192	Q91bu9 helicoverpa
10	41	80.4	192	Q8V5Q5 helicoverpa
11	41	80.4	312	Q83z37 pseudomonas
12	41	80.4	312	Q889B2 pseudomonas
13	41	80.4	317	Q6EV55 yersinia ps
14	41	80.4	322	Q8ZL19 salmonella
15	41	80.4	335	Q8Yfa7 brucella me
16	41	80.4	338	Q8Gz12 brucella su
17	41	80.4	622	Q7P1X6 chromobacte
18	41	80.4	5179	MUC2_HUMAN
19	40	78.4	117	Q6G3K0 barriolella
20	40	78.4	208	Q6FA00 acinetobact
21	40	78.4	475	Q9UFT5 caenorhabdi
22	40	78.4	593	Q6TIC6 apis mellif
23	40	78.4	593	AQ96728 apis mellif
24	40	78.4	645	Q6TIC7 apis mellif
25	40	78.4	646	AQ96727 apis mellif
26	40	78.4	821	Q96d4 caenorhabdi
27	39	76.5	310	Q8PK92 xanthomonas
28	39	76.5	313	Q8PE59 Q8PK92 xanthomonas
29	39	76.5	315	Q705P3 pseudomonas
30	39	76.5	315	Cae92907 pseudomonas
31	39	76.5	316	Q8QG67 pseudomonas

**ALIGNMENTS**

RESULT	ID	PRELIMINARY;	PRT;	AA.
1	Q8i619			
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1	Q8i619;			
1	DT	01-MAR-2003	(TREMBLrel. 23, Created)	
1	DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	
1	DE	ZIC Family	transcription factor.	
1	OS	Name=HrzicN;		
1	OC	Bukaryota; Metazoa; Chordata; Urochordata; Asciidae;		
1	OC	Stolidobranchia; Pyuridae; Halocynthia.		
1	OX	NCBI_TaxID=7729;		
1	RN	[1]		
1	RP	SEQUENCE FROM N.A.		
1	RX	Medline:22308574; PubMed:12421701;		
1	RA	Wada S.; Saiga H.; HrzicN, a new zic family gene of ascidians, plays essential roles in the neural tube and notochord development.;		
1	RT	Development 129:5397-5398 (2002).		
1	RL	EMBL; AB092643; BAC23063.1; -.		
1	DR	HSSP; P0047; ISP2.		
1	DR	GO; GO:0003634; C-nucleus; IBA.		
1	DR	GO; GO:000576; F-nucleic acid binding; IBA.		
1	DR	GO; GO:0008270; Zinc ion binding; IBA.		
1	DR	InterPro; IPR00787; Znf_C2H2.		
1	DR	PFam; PF0006; zf_C2H2; 4.		
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OX NCBI\_TAXID=180454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=PEST;  
RL Anopheles Genome Sequencing Consortium;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAB01008964; EAA438622\_1; -;  
SQ SEQUENCE 107 AA; 11827 MW; ECT388D51F12DE5 CRC64;

Query Match 82.4%; Score 42; DB 2; length 107;  
Best Local Similarity 71.4%; Pred. No. 17;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
Db 62 DCFWKVC 68

RESULT 3  
Q7R3E2 PRELIMINARY; PRT; 256 AA.  
ID Q7R3E2  
AC 07R3E2;  
DT 01-MAR-2004 (PREMBLrel. 26, Created)  
DT 01-MAR-2004 (PREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (PREMBLrel. 26, Last annotation update)  
DB GLP\_111\_2064\_2834.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
RN NCBI\_TAXID=184922;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WB\_C57  
RA Olsen G.H.; McArthur A.G.; Adam R.D.; Aley S.B.; Gillin F.D.;  
RT "Draft sequence of the Giardia lamblia genome.",  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACB0100016; EAA417761\_1; -;  
SQ REPEAT 256 AA; 2773 MW; ARBD914A8B9157A CRC64;

Query Match 82.4%; Score 42; DB 2; length 256;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
Db 52 LCYWKVC 58

RESULT 4  
TNR8 RAT STANDARD; PRT; 493 AA.  
ID P97525;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 8 precursor (CD30L receptor) (Lymphocyte activation antigen CD30).  
DE Name="tnfrsf8"; Synonyms="Cd30";  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
SQ SEQUENCE FROM N.A.  
STRAIN=WTAH; TISSUE=T-cell lymphoma;  
MEDLINE-97136705; PubMed=8982082;  
RA Alzawa S., Satoh H., Horie R., Ito K., Choi S.H., Takeuchi H.,

RN Katanabe T.;  
RT "Cloning and characterization of a cDNA for rat CD30 homolog and chromosomal assignment of the genomic gene.";  
RL Gene 182:155-162(1996).  
CC -!- FUNCTION: Receptor for TNFSF8/CD30L. May play a role in the regulation of cellular growth and transformation of activated lymphoblasts. Regulates gene expression through activation of NF-kappa-B (By similarity).  
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3 and TRAF5 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: Very low level of expression. Detected in spleen, thymus and lung. Highly expressed in HTLV-1 infected T-cell lines.  
CC -!- INDUCTION: By phytohemagglutinin (PHA) in spleen T-cells.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.

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DR EMBL; D42117; BA00699.1; -.  
DR PIR; JCS486; JCS486.  
DR HSSP; Q9296; JUMA.  
DR RGD; 3879; Thirst8.  
DR InterPro; IPR0013368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
DR Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
KW SIGNAL\_1 18  
FT CHAIN 19 493  
FT DOMAIN 19 255  
FT TRANSMEM 256 276  
FT DOMAIN 277 493  
FT REPEAT 28 66  
FT REPEAT 68 106  
FT REPEAT 107 150  
FT DISULFD 29 44  
FT DISULFD 45 58  
FT DISULFD 84 97  
FT DISULFD 87 105  
FT DISULFD 107 121  
FT DISULFD 124 142  
FT CARBOHYD 152 152  
FT CARBOHYD 179 179  
FT CARBOHYD 225 225  
SQ SEQUENCE 493 AA; 52658 MW; 40B8703BCBB7C CRC64;

Query Match 82.4%; Score 42; DB 1; length 493;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
Db 303 LCYWKVC 309

RESULT 5  
TNR8 MOUSE STANDARD; PRT; 498 AA.  
ID P97526;  
AC 060376;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 8 precursor (CD30L receptor) (Lymphocyte activation antigen CD30).

GN Name=TNfrsf8;  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Scurognathii; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=1090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Splenocyte;  
 RX MEDLINE=9613967; PubMed=8533792;  
 RA Bowen M.A., Lee R.K., Miralotti G., Nam S.Y., Podack E.R.;  
 RT "Structure and expression of murine Cd30 and its role in cytokine  
 production.",  
 RL J. Immunol. 156:442-449(1996).  
 CC -!- FUNCTION: Receptor for TNFSF8/CD30L. May play a role in the  
 regulation of cellular growth and transformation through activation of NF-  
 kappa-B (By similarity).  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3 and TRAF5 (By  
 similarity).  
 CC -!- TISSUE/LILOCAL LOCATION: Type I membrane protein (Probable).  
 CC -!- TISSUE/SPECIFICITY: Detected in thymus and in activated  
 splenocytes.  
 CC -!- INDUCTION: By concanavalin A and pokeweed mitogen in splenocytes.  
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial/  
 or send an email to license@ebi-sib.ch).  
 CC  
 DR EMBL; U25416; AAA29887.1; -.  
 DR MGD; MG119908; TNfrsf8.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6\_3.  
 DR SMART; SM0206; TNFR\_c6.  
 DR PROSITE; PS00052; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 DR KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 498 Tumor necrosis factor receptor  
 FT SIGNAL 1 18 Superfamily member 8.  
 FT REPEAT 1 18 Extracellular (Potential).  
 FT DOMAIN 19 258 Potential.  
 FT TRANSMEM 259 279 Cytosolic (Potential).  
 FT DOMAIN 280 498 Cytosolic (Potential).  
 FT REPEAT 28 66 TNFR-Cys 1.  
 FT REPEAT 68 106 TNFR-Cys 2.  
 FT REPEAT 107 150 TNFR-Cys 3.  
 FT DISURID 29 44 By similarity.  
 FT DISURID 45 58 By similarity.  
 FT DISURID 48 65 By similarity.  
 FT DISURID 69 81 By similarity.  
 FT DISURID 84 97 By similarity.  
 FT DISURID 87 105 By similarity.  
 FT DISURID 107 121 By similarity.  
 FT DISURID 128 146 By similarity.  
 FT CARBOHYD 156 156 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 183 183 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 229 229 N-linked (GlcNAc. . .) (Potential).  
 SQ SEQUENCE 498 AA; 53216 MW; 98CA2A05B38AFA71 CRC64;

O8EIJ1 PRELIMINARY; PRT; 826 AA.  
 ID O8EIJ1  
 AC O8EIJ1  
 OC O8EIJ1; TREPMBrel. 23, Created)  
 DT 01-MAR-2003 (TREPMBrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREPMBrel. 26, Last annotation update)  
 DB Periplasmic nitrate reductase.  
 GN Name=napa; Order=dicoccusName=S00848;  
 OS Shewanella oneidensis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Shewanella.  
 OX NCBI\_TaxID=70863;  
 RN [1]  
 RP SEQUENCE FROM N.A..  
 RC STRAIN=MR-1;  
 RX MEDLINE=2297686; PubMed=12368813; DOT=10.1038/nbt749;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaido E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,  
 RA Clayton R.A., Meyer T., Tsapin A., Scott J., Benan M.J.,  
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,  
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,  
 RA White O., Wolf A.M., Yamatievean J.J., Weidman J.F., Impraim M.,  
 RA Lee K., Berry J.J., Lee C.A., Mueller J.J., Kocur H.M., Gill J.,  
 RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,  
 RA Venter J.C., Nealson K.H., Fraser C.M.;  
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 Shewanella oneidensis.";  
 RL Nat. Biotechnol. 20:1118-1123 (2002).  
 DR EMBL; AE01529; AACN3924.1; -.  
 DR HSSP; B81186; ZNAP.  
 DR TIGR; S00348; -.  
 DR GO; GO:0005505; F:iron ion binding; IEA.  
 DR GO; GO:0030151; F:molybdenum ion binding; IEA.  
 DR GO; GO:0009940; F:nitrate reductase activity; IEA.  
 DR GO; GO:0015491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0042128; F:nitrate assimilation; IEA.  
 DR InterPro; IPR009010; ASP decarboxyl fold.  
 DR InterPro; IPR06656; Molybdo-Fe4S4.  
 DR InterPro; IPR06935; Molybdo\_Fe4S4.  
 DR InterPro; IPR00657; Mol\_dinuc\_bind.  
 DR InterPro; IPR00051; NAPA.  
 DR InterPro; IPR06311; Tat.  
 DR Pfam; PF00384; Molybdopterin\_1.  
 DR InterPro; IPR04379; Molybdo\_Fe4S4; 1.  
 DR Pfam; PF01568; Molybdo\_E-binding; 1.  
 DR TIGRFAMS; TIGR01706; NAPA\_1.  
 DR TIGRFAMS; TIGR01409; TAT\_signal\_seq; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 826 AA; 92474 MW; 33474D23868F6316 CRC64;

Query Match 82.4%; Score 42; DB 1; Length 826;  
 Best Local Similarity 62.5%; Pred. No. 1.e-02; Matches 5; Conservative  
 Matches 5; Indels 0; Gaps 0; Score 42; DB 2; Length 826;  
 QY 1 XCYWKVCT 8  
 DB :|||||:||| 473 NCYWTMCT 480

RN [1]  
 RP SEQUENCE FROM N.A.

Query Match 82.4%; Score 42; DB 1; Length 498;  
 Best Local Similarity 71.4%; Pred. No. 72; Matches 5; Conservative  
 Matches 5; Indels 0; Gaps 0;

Qy 1 XCYWKVC 7  
 Db 307 LCYWKAC 313



RA Kinschperf T.G., Willis D.K.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY235670; AAP14301; -.  
 DR Interpro; IPR011092; DUF1527.  
 DR Pfam; PF07513; DUF1527; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 312 AA; 33457 MW; 9C1A00C2B83FAEA4 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 312;  
 Best Local Similarity 62.5%; Pred. No. 68; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; MisMatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8  
 Db 48 ICYWLMCT 55

RESULT 12

Q889B2 PRELIMINARY; PRT; 312 AA.  
 ID Q889B2  
 AC Q889B2;  
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)  
 DE Hypothetical protein.  
 GN OrderedsNames=PSPT00849;  
 OS Pseudomonas syringae (pv. tomato).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas,  
 OC NCBI\_TaxID=323;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DG3000;  
 RX MEDLINE=2283015; PubMed=12928499; DOI=10.1073/pnas.1731982100;  
 RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,  
 RA Buell C.R., Joardar V., Lindberg M., Selengut J., Paulsen I.T.,  
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Hatt B.H.,  
 RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,  
 RA Khouri H.M., Fedorova N.B., Tian B., Russell D., Berry K.J.,  
 RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascanzo M.,  
 RA Deng W.-L., Ramos A.R., Alfonzo J.R., Cartinhour S., Chatterjee A.K.,  
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,  
 RA Bender C.L., White O.O., Fraser C.M., Collmer A., Tang X.,  
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen  
 Pseudomonas syringae pv. tomato DC3000."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).  
 DR EMBL; AE016848; AAO54384; 1; -.  
 DR TIGR; RPPT0049; -.  
 DR Interpro; IPR01092; DUF1527.  
 DR Interpro; IPR01092; DUF1527; 1.  
 KW Complete proteome; Hypothetical protein.

SEQUENCE 312 AA; 33422 MW; 1C917D8D0EB3E40F CRC64;

Query Match 80.4%; Score 41; DB 2; Length 312;  
 Best Local Similarity 62.5%; Pred. No. 68; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; MisMatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8  
 Db 48 ICYWLMCT 55

RESULT 14

Q8Z1I9 PRELIMINARY; PRT; 322 AA.  
 ID Q8Z1I9  
 AC Q8Z1I9; Q7CS5F8;  
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)  
 DE Hypothetical protein. STR4576;  
 GN OrderedsNames=SY4576; SY4576; 44273;  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OC NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT8;  
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/sj.molbio.1001607;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebastian M.,  
 RA Baker S., Basham D., Brook C., Chillingworth T., Connerton P.,  
 RA Cronin A., Davis P., Davies P., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hanlin N., Haque A., Hien T.T., Horroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 enterica serovar Typhi CT8.";  
 RT Nature 413:848-852(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TY2 / ATCC 700931;  
 RX MEDLINE=22531367; PubMed=12644504;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G. F., Rose D. J.,  
 RA Burland V., Kodama Y., Schwartz D. C., Blattner F. R.,  
 RT and CIRB.;  
 RA J. Bacteriol. 185:2230-2237 (2003).  
 DR EMBL; AE016848; AAO1731; 1; -.  
 DR Interpro; IPR01092; DUF1527.  
 DR Pfam; PF07513; DUF1527; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 322 AA; 34841 MW; 8E08C95F19237648 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 322;  
 Best Local Similarity 62.5%; Pred. No. 70; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; MisMatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKVCT 8  
 Db 48 ICYWLMCT 55

RESULT 15  
 Q8YF47 PRELIMINARY; PRT; 335 AA.  
 ID Q8YF47;  
 AC 08YF47;  
 DT 01-MAR-2002 (TREMBREL, 20, Created)  
 DT 01-MAR-2004 (TREMBREL, 26, Last annotation update)  
 DE TRANSCRIPTIONAL REGULATOR, ARAC FAMILY.  
 GN OrderedLocusName=BMEI1615;  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16 / ATCC 23456 / Biotype 1;  
 RX MEDLINE=20020109; PubMed=1156688; DOI=10.1073/pnas.221575398;  
 RA DelVecchio V.G., Kapratchai V., Redkar R.J., Patra G., Mujer C., Los T.,  
 RA Ivanova N., Anderson J., Bhattacharyya A., Lykidis A., Roznik G.,  
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldzman E.,  
 RA Selkow E., Elzer P.H., Hagiw S., O'Callaghan D., Letesson J.-J.,  
 RA Hasekorn R., Kypride R.; Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 RT Brucella melitensis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
 CC !- SIMILARITY: Contain 1 HTH arac/CysLS-type DNA-binding domain.  
 DR EMBL; AED009597; AAH52796.1; -.  
 DR PIR; A13453; A13453.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR009057; Homeodomain\_like.  
 DR InterPro; IPR00005; HTHarAC.  
 DR InterPro; IPR02818; ThhJ/Pfif1.  
 DR Pfam; PF01965; DJT-1\_PfPf1; 1.  
 DR Pfam; PF0165; HTH\_arac; 2.  
 DR PRINTS; PR00032; HTHarAC.  
 DR SMART; SM00342; HTH\_arac; 1.  
 DR PROSITE; PS01124; HTH\_ARAC\_FAMILY\_2; 1.  
 DR Complete\_proteome; DNA-binding; Transcription regulation.  
 KW SEQUENCE 335 AA; 37076 MW; F66631P5237P38D6 CRC64;  
 SQ  
 Query Match 80.4%; Score 41; DB 2; Length 335;  
 Best Local Similarity 62.5%; Pred. No. 72;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XCYWKVCT 8  
 Db 59 RCWKVCT 66

Search completed: November 18, 2004, 16:20:53  
 Job time : 67 secs

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GenCore version 5.1.6

Om protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 37 Seconds  
 (without alignments)  
 20.804 Million cell updates/sec

Title: SEQ1  
 perfect score: 51  
 Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX  
 Gapop 10.0 , Gpext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Maximum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	42	82.4	JC5486	membrane glycoprotein CD30 homolog precursor - rat
2	41	80.4	JAF1031	hypothetical protein
3	41	80.4	AJ3453	hypothetical protein
4	41	80.4	A413932	transcription regu-
5	40	78.4	T33943	mucin 2 precursor,
6	39	74.5	F59101	hypothetical prote-
7	38	74.5	A54895	mucin 2, intestine
8	38	74.5	T00568	hypothetical prote-
9	37	72.5	12	urotensin II - ion
10	37	72.5	JSD423	urotensin II-A pep
11	37	72.5	S42765	urotensin II - tel
12	37	72.5	JSD424	C/Species: <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi
13	37	72.5	PQ0445	A/Note: this species has also been called <i>Salmonella</i> typhi
14	37	72.5	S10706	C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
15	37	72.5	I25	C/Accession: AF1031
16	37	72.5	150498	R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.N.; Churcher, S.J.; Moulé, S.; O'Gara, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, T.J.; Compton, P.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 848-852, 2001
17	37	72.5	253	A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; T09574
18	37	72.5	2	A/Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar
19	37	72.5	1375	A/Reference number: AB0502; PMID:21534997; PMID:11677608
20	36	70.6	451	R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.N.; Churcher, S.J.; Moulé, S.; O'Gara, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, T.J.; Compton, P.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 848-852, 2001
21	36	70.6	627	A/Accession: AF031
22	36	70.6	2	A/Status: Preliminary
23	36	70.6	1360	A/Molecule type: DNA
24	35	68.6	69	A/Residues: 1-322 <PAR>
25	35	68.6	2	A/Cross-references: GB:AL1513382; PIDN:CA09351.1; PID:g16505351; GSPDB:GN00176
26	35	68.6	506	C/Genetics:
27	35	68.6	2	A/Gene: SIV576
28	35	68.6	523	A/HB445
29	35	68.6	2	

**ALIGNMENTS**

Query Match 80.4%; Score 41; DB 2; Length 322;  
 Best Local Similarity 62.5%; Pred. No. 22; Indels 1; Gaps 0;  
 Matches 5; Conservative 2; Mismatches 1;

Qy 1 XCYWKCCT 8  
 Db 48 ICYWLMCT 55

RESULT 3

A13453 transcription regulator, arac family BMEI1615 [imported] - *Brucella melitensis* (strain 1) C;Species: *Brucella melitensis*  
 C;Accession: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 R;DeVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Muier, C.; Ios, T.; Ivanova, N.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Jeffress, J.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis* A;Reference number: AD3252; PMID:11756688  
 A;Accession: A13453  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-335 <KUR>  
 A;Experimental source: strain 16M  
 C;Genetics:  
 A;Gene: BMEI1615  
 A;Map position: I

Query Match 80.4%; Score 41; DB 2; Length 335;  
 Best Local Similarity 62.5%; Pred. No. 23; Indels 1; Gaps 0;  
 Matches 5; Conservative 2; Mismatches 1;

Qy 1 XCYWKCCT 8  
 Db 59 RCWKICKT 66

RESULT 4

A43932 mucin 2 precursor, intestinal - human (fragments)  
 N;Alternate names: mucin SMUC-41  
 C;Species: Homo sapiens (man)  
 C;Date: 10-May-1993 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004  
 C;Accession: A43932; A45106; B45106; A4392; B33532; A62257; PQ028; PQ0329  
 R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.  
 J. Biol. Chem. 269, 2440-2446, 1994  
 A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A43963; MUID:94122002; PMID:8300571  
 A;Accession: A43963  
 A;Molecule type: mRNA  
 A;Residues: 1-639 <GUI>  
 A;Genetics:  
 A;Gene: GRB:MUC2  
 A;Cross-references: OMIM:158370  
 A;Map position: 1P15.5;1P5.5  
 C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von Willebrand factor tandem repeat  
 C;Keywords: glycoprotein; intestine; tandem repeat homology <WMC>  
 F;2766-2834//Domain: von Willebrand factor type C repeat homology <WMC>  

Query Match 80.4%; Score 41; DB 2; Length 3020;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 3; Mismatches 1;

Qy 1 XCYWKCCT 8  
 Db 1237 FCYWBIC 1243

RESULT 5

T33943 hypothetical protein C01B4.7 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T33943  
 R;Smith, A.; Wamsley, P.; Pronick, W.  
 submitted to the EMBL Data Library, February 1999  
 A;Description: The sequence of *C. elegans* cosmid C01B4.  
 A;Reference number: 221443  
 A;Accession: T33943  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-475 <SM1>  
 A;Cross-references: GB:M94131; NID:gi:186395; PNIN:AA5A59163.1; PID:gi186396  
 A;Experimental source: colon  
 A;Note: sequence extracted from NCBI backbone (NCBIP:116706)  
 A;Note: conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 2037-3020 <GU3>  
 A;Cross-references: GB:M94132; NID:gi:186397; PNIN:AA5A59164.1; PID:gi186398  
 A;Experimental source: colon  
 A;Note: sequence extracted from NCBI backbone (NCBIP:116698)  
 J. Clin. Invest. 88, 1005-1013, 1991  
 A;Gene: CESP:C01B4.7



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US-10-427-160A-22 ; Sequence 22, Application US/10427160A  
; Publication No. US20040110296A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirma Therapeutics, Inc.  
; APPLICANT: Vargese, Chandra  
; APPLICANT: Haebel, Peter  
; APPLICANT: Wang, Weinan  
; APPLICANT: Chen, Tongqian  
; TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery  
; CURRENT APPLICATION NUMBER: US10/427,160A  
; CURRENT FILING DATE: 2003-04-30  
; PRIORITY FILING DATE: 2002-05-17  
; PRIORITY APPLICATION NUMBER: US 60/292,217  
; PRIORITY FILING DATE: 2001-05-18  
; PRIORITY APPLICATION NUMBER: US 60/362,016  
; PRIORITY FILING DATE: 2002-03-06  
; PRIORITY APPLICATION NUMBER: US 60/306,883  
; PRIORITY FILING DATE: 2001-07-20  
; PRIORITY APPLICATION NUMBER: US 60/292,217  
; PRIORITY FILING DATE: 2001-08-13  
; PRIORITY APPLICATION NUMBER: PCT/US 03/05346  
; PRIORITY FILING DATE: 2003-02-20  
; PRIORITY APPLICATION NUMBER: PCT/US 03/05028  
; PRIORITY FILING DATE: 2003-02-20  
; PRIORITY APPLICATION NUMBER: US 60/311,865  
; PRIORITY FILING DATE: 2001-08-13  
; PRIORITY APPLICATION NUMBER: PCT/US 03/05346  
; PRIORITY FILING DATE: 2003-02-20  
; PRIORITY APPLICATION NUMBER: RNA Interference Mediated Inhibition of Gene Expression Using  
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (sINA)  
; FILE REFERENCE: 400/114 (MBB03-465)  
; CURRENT APPLICATION NUMBER: US/10/444,853A  
; CURRENT FILING DATE: 2003-05-23  
; PRIORITY APPLICATION NUMBER: US 10/417,012  
; PRIORITY FILING DATE: 2003-04-16  
; PRIORITY APPLICATION NUMBER: PCT/US3/05346  
; PRIORITY FILING DATE: 2003-02-20  
; PRIORITY APPLICATION NUMBER: PCT/US03/05028  
; PRIORITY FILING DATE: 2003-02-20  
; PRIORITY APPLICATION NUMBER: US 60/358,580  
; PRIORITY FILING DATE: 2002-02-20  
; PRIORITY APPLICATION NUMBER: US 60/363,124  
; PRIORITY FILING DATE: 2002-03-11  
; PRIORITY APPLICATION NUMBER: US 60/386,782  
; PRIORITY FILING DATE: 2002-06-06  
; PRIORITY APPLICATION NUMBER: US 60/406,784  
; PRIORITY FILING DATE: 2003-08-29  
; PRIORITY APPLICATION NUMBER: US 60/408,378  
; PRIORITY FILING DATE: 2003-09-05  
; PRIORITY APPLICATION NUMBER: US 60/409,293  
; PRIORITY FILING DATE: 2002-09-09  
; PRIORITY APPLICATION NUMBER: US 60/440,129  
; PRIORITY FILING DATE: 2003-01-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 22  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Ser stands for optional Serine for coupling  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: Phe stands for optional D isomer for stability  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Trp stands for optional D isomer for stability  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Synthetic peptide  
; US-10-427-160A-22

Query Match 92.2%; Score 47; DB 16; Length 9;  
; Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
; QY 1 XCYWVKT 8  
; :||| |  
; 2 FCYWKTCT 9  
; Db

RESULT 3  
; Sequence 515, Application US/10444853A  
; Publication No. US2004019266A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirma Therapeutics, Inc.  
; APPLICANT: Haebel, Peter

US-10-444-853A-515  
; Query Match 92.2%; Score 47; DB 17; Length 9;  
; Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
; QY 1 XCYWVKT 8  
; :||| |  
; 2 FCYWKTCT 9  
; Db

RESULT 4  
; Sequence 4, Application US/10258766A1  
; Publication No. US2004136507A1  
; GENERAL INFORMATION:  
; APPLICANT: BioSynthesis, Inc.

```

; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816_17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1).-(1)
; OTHER INFORMATION: Arg(Pmc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3).-(3)
; OTHER INFORMATION: Asp(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5).-(5)
; OTHER INFORMATION: DTYr(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5).-(5)
; OTHER INFORMATION: Asp(beta-OAll)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5).-(6)
; OTHER INFORMATION: Lys(Mtt)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7).-(7)
; OTHER INFORMATION: Dpme
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9).-(9)
; OTHER INFORMATION: Tyr(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8).-(8)
; OTHER INFORMATION: Cys(Acm)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11).-(11)
; OTHER INFORMATION: DTrp(tBoc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (11).-(11)
; OTHER INFORMATION: Lys(tBoc)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12).-(12)
; OTHER INFORMATION: Thr(OtBu)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13).-(13)
; OTHER INFORMATION: Cys(Acm)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14).-(14)
; OTHER INFORMATION: Thr(OtBu)-O-BESIN
US-10-258-766A-1

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2,3; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; MisMatch 1; DelMatch 0; InsertMatch 0;

QY      1 XCYWKVCT 8
Db      7 FCYWKCT 14

```

```

RESULT 6
US-10-258-766A-7
; Sequence 7 Application US/10/258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: BioSyrthma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8).-(13)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC_FEATURE

```

```

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2,3; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; MisMatch 1; DelMatch 0; InsertMatch 0;

QY      1 XCYWKVCT 8
Db      7 FCYWKCT 14

```

```

RESULT 6
US-10-258-766A-7
; Sequence 7 Application US/10/258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: BioSyrthma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816_17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8).-(13)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC_FEATURE

```

LOCATION: (1)..(5)  
 OTHER INFORMATION: Amide bond between residues 1 and 5

FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (6)..(6)  
 OTHER INFORMATION: D<sup>Tyr</sup>  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (7)..(7)  
 OTHER INFORMATION: NH-DTPA  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (9)..(9)  
 OTHER INFORMATION: Lys  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (10)..(10)  
 OTHER INFORMATION: D<sup>Phe</sup>  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (11)..(11)  
 OTHER INFORMATION: Lys(tBoc)  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (12)..(12)  
 OTHER INFORMATION: Thr(OtBu)  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (13)..(13)  
 OTHER INFORMATION: Cys(AcM)  
 FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (14)..(14)  
 OTHER INFORMATION: Thr-OH

US-10-258-766A-8

Query Match 92.2%; Score 47; DB 16; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.3; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; MisMatches 1;

QY 1 XCYWKVCT 8  
 Db 7 FCYWKCT 14

RESULT 7

Sequence 8, Application US/10258766A  
 Publication No. US20040136907A1

GENERAL INFORMATION:  
 APPLICANT: Biosyntenna, Inc.  
 TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES  
 FILE REFERENCE: 717816.17  
 CURRENT APPLICATION NUMBER: US/10/258,766A  
 NUMBER OF SEQ ID NOS: 14  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 8

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:  
 NAME/KEY: MOD\_RES  
 LOCATION: (1)..(1)  
 OTHER INFORMATION: Arg(Pmc)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (4)..(4)

OTHER INFORMATION: D<sup>Tyr</sup>(OtBu)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (6)..(6)

OTHER INFORMATION: Lys(Mtt)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (7)..(7)

OTHER INFORMATION: D<sup>Phe</sup>

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (8)..(8)

OTHER INFORMATION: Cys(Acm)

LOCATION: (8)..(8)

OTHER INFORMATION: Cys(Acm)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (9)..(9)

OTHER INFORMATION: Tyr(OtBu)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (10)..(10)

OTHER INFORMATION: D<sup>Tyr</sup>(tBoc)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (11)..(11)

OTHER INFORMATION: Lys(tBoc)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (12)..(12)

OTHER INFORMATION: Thr(OtBu)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (13)..(13)

OTHER INFORMATION: Cys(AcM)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (14)..(14)

OTHER INFORMATION: Thr(OtBu)-O-RESIN

US-10-258-766A-8

Query Match 92.2%; Score 47; DB 16; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.3; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; MisMatches 1;

QY 1 XCYWKVCT 8  
 Db 7 FCYWKCT 14

RESULT 8

Sequence 13, Application US/10258766A  
 Publication No. US20040136907A1

GENERAL INFORMATION:  
 APPLICANT: Biosyntenna, Inc.  
 TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES  
 FILE REFERENCE: 717816.17  
 CURRENT APPLICATION NUMBER: US/10/258,766A  
 CURRENT FILING DATE: 2002-10-25  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 13

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (4)..(4)

OTHER INFORMATION: D<sup>Tyr</sup>(OtBu)

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (7)..(7)

OTHER INFORMATION: D<sup>Phe</sup>

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (10)..(10)

OTHER INFORMATION: D<sup>Tyr</sup>

FEATURE:  
 NAME/KEY: MOD\_RES

LOCATION: (14)..(14)

OTHER INFORMATION: Thr(OtBu)-O-RESIN

FEATURE:  
 NAME/KEY: DISUFDID

LOCATION: (8)..(13)

OTHER INFORMATION:

```

; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Amide bond between residues 1 and 5
US-10-258-766A-13

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
OQ :||||| 1 XCYWKVCT 8
Db :||||| 7 FCYWKCT 14

RESULT 9
US-10-258-766A-14
; Sequence 14, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthesma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816_17
; CURRENT APPLICATION NUMBER: US10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE: NAME/KEY: DISULFID
LOCATION: (1)..(6)
OTHER INFORMATION:
FEATURE: NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr
FEATURE: NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: NH-DTPA
FEATURE: NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: Lys
FEATURE: NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DPhe
FEATURE: NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp
FEATURE: NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr(OtBu)-OH
FEATURE: NAME/KEY: MISC_FEATURE
LOCATION: (1)..(15)
OTHER INFORMATION: Amide bond between residues 1 and 5
US-10-258-766A-14

Query Match 92.2%; Score 47; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e-06; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
OQ :||||| 2 CYWKVCT 8
Db :||||| 1 CYWKCT 7

RESULT 11
US-10-258-766A-10
; Sequence 10, Application US/10258766A
; Publication No. US20040136907A1
; GENERAL INFORMATION:
; APPLICANT: Biosynthesma, Inc.
; TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
; FILE REFERENCE: 717816_17
; CURRENT APPLICATION NUMBER: US/10/258,766A
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 10
; LENGTH: 7
; TYPE: PRT

RESULT 10

```

ORGANISM: Homo sapiens  
 FEATURE: MOD\_RES  
 LOCATION: (1)..(1)  
 OTHER INFORMATION: Cys (Acm)

FEATURE: MOD\_RES  
 LOCATION: (2)..(2)  
 OTHER INFORMATION: Tyr (OtBu)

FEATURE: MOD\_RES  
 LOCATION: (3)..(3)  
 OTHER INFORMATION: DTrp (tBoc)

FEATURE: MOD\_RES  
 NAME/KEY: MOD\_RES  
 LOCATION: (4)..(4)  
 OTHER INFORMATION: Lys (tBoc)

FEATURE: MOD\_RES  
 NAME/KEY: MOD\_RES  
 LOCATION: (5)..(5)  
 OTHER INFORMATION: Thr (OtBu)

FEATURE: MOD\_RES  
 NAME/KEY: MOD\_RES  
 LOCATION: (6)..(6)  
 OTHER INFORMATION: Cys (Acm)

FEATURE: MOD\_RES  
 NAME/KEY: MOD\_RES  
 LOCATION: (7)..(7)  
 OTHER INFORMATION: Thr (ol) (OtBu)-O-RESIN

US-10-258-766A-10

Query Match 90.2%; Score 46; DB 16; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+06; 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;

Qy 2 CYWKVCT 8  
 Db 1 CYWKVCT 7

RESULT 12  
 US-10-258-766A-12

; Sequence 12. Application US/10258766A  
 ; Publication No. US20040136907A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BioSynthesis, Inc.  
 ; TITLE OF INVENTION: (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES  
 ; FILE REFERENCE: 717816.17  
 ; CURRENT APPLICATION NUMBER: US10/10258,766A  
 ; CURRENT FILING DATE: 2002-10-25  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 12  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: DISURPID  
 ; LOCATION: (1)..(6)  
 ; OTHER INFORMATION:  
 ; FEATURE:  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (1)..(1)  
 ; OTHER INFORMATION: Cys (Acm)  
 ; FEATURE:  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (2)..(2)  
 ; OTHER INFORMATION: Tyr (OtBu)  
 ; FEATURE:  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (3)..(3)  
 ; OTHER INFORMATION: DTrp (tBoc)

RESULT 13  
 US-10-036-869-13

Query Match 90.2%; Score 46; DB 16; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+06; 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;

Qy 2 CYWKVCT 8  
 Db 1 CYWKVCT 7

RESULT 13  
 US-10-036-869-13

; Sequence 13. Application US/10036869  
 ; Publication No. US20020151516A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mixson, James A  
 ; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
 ; STREET: 1220 Market Street, P.O. Box 2207  
 ; CITY: Wilmington  
 ; STATE: Delaware  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19899  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/035,869  
 ; FILING DATE: 23-Nov. US20020151516A-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/985,526  
 ; FILING DATE: <Unknown>  
 ; FILING DATE: 08/08/2000  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMorrow Jr., Robert G  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (302) 658-9141  
 ; TELEFAX: (302) 658-5613  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-036-869-13

Query Match 90.2%; Score 46; DB 13; Length 9;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+06; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0;

QY 1 XCYWKVC 7  
 QY 2 :||||| FCYWKVC 8  
 Db

---

RESULT 14  
 US-10-300-083-3  
 ; Sequence 3: Application US/10300083  
 Publication No. US20030153502A1  
 GENERAL INFORMATION:  
 APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA  
 TITLE OF INVENTION: SYNTHETIC APPROACH TO DESIGNED CHEMICAL  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MEETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
 STREET: 119 N. St. Paul Street, Suite 203  
 CITY: Minneapolis  
 STATE: Minnesota  
 COUNTRY: U.S.A.  
 ZIP: 55401  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/300,083  
 FILING DATE: 20-NO. US20030153502A1-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/194,296  
 FILING DATE: 15-OCT-1999  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MCCORMACK, MYRA M.  
 REGISTRATION NUMBER: 35,602  
 REFERENCE/DOCKET NUMBER: 110.003130220  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-305-1225  
 TELEFAX: 612-305-1228  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 33 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-10-300-083-3

Query Match 90.2%; Score 46; DB 14; Length 33;  
 Best Local Similarity 85.7%; Pred. No. 6 4; Matches 6;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7  
 QY 2 :||||| FCYWKVC 8  
 Db

---

RESULT 15  
 US-10-036-869-15  
 ; Sequence 15: Application US/10036869  
 Publication No. US20020151516A1  
 GENERAL INFORMATION:  
 APPLICANT: MIXSON, James A  
 TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA ENCODING ANTI-ANGIogenic PEPTIDES AND THEIR USE IN GENE THERAPY  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:

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Creation date: 12-02-2004

Indexing Officer: MMOHAMMED1 - MENEN MOHAMMED

Team: OIPEScanning

Dossier: 10021002

Legal Date: 10-14-2004

No.	Doccode	Number of pages
1	SRNT	44

Total number of pages: 44

Remarks:

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